



-1-

SEQUENCE LISTING

<110> Gray et al.

<120> MACROPHAGE DERIVED CHEMOKINE (MDC), MDC ANALOGS, MDC INHIBITOR SUBSTANCES, AND USES THEREOF

<130> 27866/34810

<140> 09/509,165

<141> 2000-06-12

<150> 09/067,447

<151> 1998-04-28

<150> 08/939,107

<151> 1997-09-26

<150> 08/660,542

<151> 1996-06-07

<150> 08/558,658

<151> 1995-11-16

<150> 08/479,620

<151> 1995-06-07

<160> 46

<170> PatentIn Ver. 2.0

<210> 1

<211> 2923

<212> DNA

<213> Homo sapiens - human MDC cDNA

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<222> (20)..(298)

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<222> (92)..(298)

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Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val

-20

-15

ctc gtc ctc ctt gct gtg gcg ctt caa gca act gag gca ggc ccc tac 100  
Leu Val Leu Ala Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr

-10

-5

1

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MAR 12 2002  
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ggc gcc aac atg gaa gac agc gtc tgc tgc cgt gat tac gtc cgt tac 148  
Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr  
5 10 15

cgt ctg ccc ctg cgc gtg gtg aaa cac ttc tac tgg acc tca gac tcc 196  
Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser  
20 25 30 35

tgc ccg agg cct ggc gtg gtg cta acc ttc agg gat aag gag atc 244  
Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile  
40 45 50

tgt gcc gat ccc aga gtg ccc tgg gtg aag atg att ctc aat aag ctg 292  
Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu  
55 60 65

agc caa tgaagagcct actctgatga ccgtggcctt ggctcctcca ggaaggctca 348  
Ser Gln

ggagccctac ctccctgcca ttatacgatgc tccccgccag aagcctgtgc caactctcg 408

cattccctga tctccatccc tgtggctgtc acccttggtc acctccgtgc tgtcaactgcc 468

atctcccccc tgaccctct aaccatccct ctgcctccct ccctgcagtc agagggctct 528

gttcccatca gcgattcccc tgcttaaacc ctccatgac tccccactgc cctaagctga 588

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<211> 93  
<212> PRT  
<213> Homo sapiens - human MDC

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-20 -15 -10

Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu  
-5 -1 1 5

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg  
10 15 20

Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly  
25 30 35 40

Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg  
45 50 55

Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln  
60 65

*0*  
<210> 3  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer JHSP6

<400> 3  
gacactatacg aatagggc 18

<210> 4  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer M13

<400> 4  
gtaaaaacgac ggccagt 17

<210> 5  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer T3.1

<400> 5  
aattaaccct cactaaaggg

20

<210> 6  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer T7.1

<400> 6  
gtaatacgac tcactatagg gc

22

<210> 7  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer 390-1F

<400> 7  
tctatctaga ggcccctacg gcgccaaat ggaag

35

<210> 8  
<211> 33  
<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer 390-2R

<400> 8  
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33

<210> 9  
<211> 29  
<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer 390-4R

<400> 9  
aatggatcca cagcacggag gtgaccaag

29

<210> 10

<211> 31

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer 390-3R

<400> 10

agtcaagctt agggcactct gggatcggca c

31

<210> 11

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390-FX2

<400> 11

tatcgatcc tggatcccg tggccctac ggcgcacaaca tggaa

45

<210> 12

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer GEX5

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gaaatccagc aagtatata tag ca

22

<210> 13

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390-Pel

<400> 13

attgcatgg ccggccctta cggcgccaa ac atggaa

36

<210> 14

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390RcH

<400> 14

gaccaagctt gagacataca ggacagagca

30

<210> 15

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390RcX

<400> 15

tggatctaga agttggcaca ggcttctgg

29

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer DC03

<400> 16

cgaaatatac acgactcact

20

<210> 17

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer  
390mycRX

<400> 17

tggatctaga tcaattcaag tcctcctcgc tgatcagctt ctgctttgg ctcagcttat 60

tgagaat

67

<210> 18

<211> 99

<212> PRT

<213> Homo sapiens - Hu MCP-3

<400> 18

Met Lys Ala Ser Ala Ala Leu Leu Cys Leu Leu Leu Thr Ala Ala Ala  
-20 -15 -10

Phe Ser Pro Gln Gly Leu Ala Gln Pro Val Gly Ile Asn Thr Ser Thr  
-5 1 5

Thr Cys Cys Tyr Arg Phe Ile Asn Lys Lys Ile Pro Lys Gln Arg Leu  
10 15 20 25

Glu Ser Tyr Arg Arg Thr Thr Ser Ser His Cys Pro Arg Glu Ala Val  
30 35 40

Ile Phe Lys Thr Lys Leu Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln  
45 50 55

Lys Trp Val Gln Asp Phe Met Lys His Leu Asp Lys Lys Thr Gln Thr  
60 65 70

Pro Lys Leu  
75

<210> 19

<211> 99

<212> PRT

<213> Homo sapiens - Hu MCP-1

<400> 19

Met Lys Val Ser Ala Ala Leu Leu Cys Leu Leu Leu Ile Ala Ala Thr  
-20 -15 -10

Phe Ile Pro Gln Gly Leu Ala Gln Pro Asp Ala Ile Asn Ala Pro Val  
-5 1 5

Thr Cys Cys Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu  
10 15 20 25

Ala Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val  
30 35 40

Ile Phe Lys Thr Ile Val Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln  
45 50 55

Lys Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr  
60 65 70

Pro Lys Thr  
75

<210> 20

<211> 76

<212> PRT

<213> Homo sapiens - Hu MCP-2

<400> 20

Gln Pro Asp Ser Val Ser Ile Pro Ile Thr Cys Cys Phe Asn Val Ile  
1 5 10 15

Asn Arg Lys Ile Pro Ile Gln Arg Leu Glu Ser Tyr Thr Arg Ile Thr  
20 25 30

Asn Ile Gln Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Lys Arg Gly  
35 40 45

Lys Glu Val Cys Ala Asp Pro Lys Glu Arg Trp Val Arg Asp Ser Met  
50 55 60

Lys His Leu Asp Gln Ile Phe Gln Asn Leu Lys Pro  
65 70 75

*P* | |  
<210> 21

<211> 91

<212> PRT

<213> Homo sapiens - RANTES

<400> 21

Met Lys Val Ser Ala Ala Ala Leu Ala Val Ile Leu Ile Ala Thr Ala  
-20 -15 -10

Leu Cys Ala Pro Ala Ser Ala Ser Pro Tyr Ser Ser Asp Thr Thr Pro  
-5 1 5

Cys Cys Phe Ala Tyr Ile Ala Arg Pro Leu Pro Arg Ala His Ile Lys  
10 15 20 25

Glu Tyr Phe Tyr Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val Phe  
30 35 40

Val Thr Arg Lys Asn Arg Gln Val Cys Ala Asn Pro Glu Lys Lys Trp  
45 50 55

Val Arg Glu Tyr Ile Asn Ser Leu Glu Met Ser  
60 65

<210> 22

<211> 91

<212> PRT

<213> Homo sapiens - MIP-1 beta

<400> 22

Met Lys Leu Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala  
-20 -15 -10

Phe Cys Ser Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr  
-5 1 5

Ala Cys Cys Phe Ser Tyr Thr Arg Glu Ala Ser Ser Asn Phe Val Val  
10 15 20 25

Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val Phe  
30 35 40

Gln Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser Trp  
45 50 55

Val Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn  
60 65

*P* / <210> 23

<211> 92

<212> PRT

<213> Homo sapiens - MIP-1 alpha

<400> 23

Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala  
-20 -15 -10

Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala  
-5 1 5 10

Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala  
15 20 25

Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe  
30 35 40

Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp  
45 50 55

Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala  
60 65 70

<210> 24

<211> 96

<212> PRT

<213> Homo sapiens - I-309

<400> 24

Met Gln Ile Ile Thr Thr Ala Leu Val Cys Leu Leu Leu Ala Gly Met  
-20 -15 -10

Trp Pro Glu Asp Val Asp Ser Lys Ser Met Gln Val Pro Phe Ser Arg  
-5 1 5 10

Cys Cys Phe Ser Phe Ala Glu Gln Glu Ile Pro Leu Arg Ala Ile Leu  
15 20 25

Cys Tyr Arg Asn Thr Ser Ser Ile Cys Ser Asn Glu Gly Leu Ile Phe  
30 35 40

Lys Leu Lys Arg Gly Lys Glu Ala Cys Ala Leu Asp Thr Val Gly Trp  
45 50 55

Val Gln Arg His Arg Lys Met Leu Arg His Cys Pro Ser Lys Arg Lys  
60 65 70

<210> 25

<211> 93

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Human MDC Analog

<220>

<221> misc\_feature

<222> (24)

<223> Xaa = arg, gly, ala, val, leu, ile,  
pro, ser, thr, phe, tyr, trp, aspartate,  
glutamate, asn, gln, cys, or met

<220>

<221> misc\_feature

<222> (27)

<223> Xaa = lys, gly, ala, val, leu, ile, pro, ser, thr, phe, tyr, trp,  
aspartate, glutamate, asn, gln, cys, or met

<220>

<221> misc\_feature

<222> (30)

<223> Xaa = tyr, ser, lys, arg, his, aspartate, glutamate, asn, gln, or  
cys

<220>

<221> misc\_feature

<222> (50)

<223> Xaa = glu, lys, arg, his, gly, or ala

<220>  
<221> misc\_feature  
<222> (59)  
<223> Xaa = trp, ser, lys, arg, his, aspartate, glutamate, asn, gln, or  
cys

<220>  
<221> misc\_feature  
<222> (60)  
<223> Xaa = val, ser, lys, arg, his, aspartate, glutamate, asn, gln, or  
cys

<400> 25  
Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val Leu Val Leu Ala  
-20 -15 -10

Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu  
-5 1 5

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Xaa  
10 15 20

Val Val Xaa His Phe Xaa Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly  
25 30 35 40

Val Val Leu Leu Thr Phe Arg Asp Lys Xaa Ile Cys Ala Asp Pro Arg  
45 50 55

Val Pro Xaa Xaa Lys Met Ile Leu Asn Lys Leu Ser Gln  
60 65

*01*  
<210> 26  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer 390-7F

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tattggatcc gttctagctc cctgttctcc 30

<210> 27  
<211> 31  
<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer 390-8R

<400> 27

ccaagaattc ctgcagccac tttctggct c

31

<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer ARA1

<400> 28

gcgactctc actgtttctc

20

<210> 29

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer ARA2

<400> 29

cacaggaaac agctatgacc

20

<210> 30

<211> 70

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human MDC analog

<400> 30

Leu Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp  
1 5 10 15

Tyr Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp  
20 25 30

Thr Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg  
35 40 45

Asp Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile  
50 55 60

Leu Asn Lys Leu Ser Gln

65 70

<210> 31  
<211> 69  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Human MDC analog

<400> 31  
Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr  
1 5 10 15

Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr  
20 25 30

Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp  
35 40 45

Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Tyr Leu Lys Met Ile Leu  
50 55 60

Asn Lys Leu Ser Gln  
65

<210> 32  
<211> 69  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence: Human MDC analog

<400> 32  
Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr  
1 5 10 15

Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys Glu Tyr Phe Tyr Thr  
20 25 30

Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp  
35 40 45

Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu  
50 55 60

Asn Lys Leu Ser Gln  
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<210> 33

<211> 1677

<212> DNA

<213> Homo sapiens - human CCR4 cDNA

<220>

<221> CDS

<222> (183) .. (1262)

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tctctcattt cccttctcct tctccctcag tctccacatt caacattgac aagtccattc 120

agaaaagcaa gctgcttctg gttggggcca gacctgcctt gaggagcctg tagagttaaa 180

aa atg aac ccc acg gat ata gca gat acc acc ctc gat gaa agc ata 227  
Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile  
1 5 10 15

tac agc aat tac tat ctg tat gaa agt atc ccc aag cct tgc acc aaa 275  
Tyr Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys  
20 25 30

gaa ggc atc aag gca ttt ggg gag ctc ttc ctg ccc cca ctg tat tcc 323  
Glu Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser  
35 40 45

ttg gtt ttt gta ttt ggt ctg ctt gga aat tct gtg gtg gtt ctg gtc 371  
Leu Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val  
50 55 60

ctg ttc aaa tac aag cgg ctc agg tcc atg act gat gtg tac ctg ctc 419  
Leu Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu  
65 70 75

aac ctt gcc atc tcg gat ctg ctc ttc gtg ttt tcc ctc cct ttt tgg 467  
Asn Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp  
80 85 90 95

ggc tac tat gca gca gac cag tgg gtt ttt ggg cta ggt ctg tgc aag 515  
Gly Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys  
100 105 110

atg att tcc tgg atg tac ttg gtg ggc ttt tac agt ggc ata ttc ttt 563  
Met Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe  
115 120 125

gtc atg ctc atg agc att gat aga tac ctg gcg ata gtg cac gcg gtg 611  
Val Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val  
130 135 140

ttt tcc ttg agg gca agg acc ttg act tat ggg gtc atc acc agt ttg 659  
Phe Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu  
145 150 155

gct aca tgg tca gtg gct gtg ttc gcc tcc ctt cct ggc ttt ctg ttc 707  
Ala Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe  
160 165 170 175

agc act tgt tat act gag cgc aac cat acc tac tgc aaa acc aag tac 755  
Ser Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr  
180 185 190

tct ctc aac tcc acg acg tgg aag gtt ctc agc tcc ctg gaa atc aac 803  
Ser Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn  
195 200 205

att ctc gga ttg gtg atc ccc tta ggg atc atg ctg ttt tgc tac tcc 851  
Ile Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser  
210 215 220

atg atc atc agg acc ttg cag cat tgt aaa aat gag aag aag aac aag 899  
Met Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys  
225 230 235

gcg gtg aag atg atc ttt gcc gtg gtc ctc ttc ctt ggg ttc tgg 947  
Ala Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp  
240 245 250 255

aca cct tac aac ata gtg ctc ttc cta gag acc ctg gtg gag cta gaa 995  
Thr Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu  
260 265 270

gtc ctt cag gac tgc acc ttt gaa aga tac ttg gac tat gcc atc cag 1043  
Val Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln  
275 280 285

gcc aca gaa act ctg gct ttt gtt cac tgc tgc ctt aat ccc atc atc 1091  
Ala Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile  
290 295 300

tac ttt ttt ctg ggg gag aaa ttt cgc aag tac atc cta cag ctc ttc 1139  
Tyr Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe  
305 310 315

aaa acc tgc agg ggc ctt ttt gtg ctc tgc caa tac tgt ggg ctc ctc 1187  
Lys Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu  
320 325 330 335

caa att tac tct gct gac acc ccc agc tca tct tac acg cag tcc acc 1235  
Gln Ile Tyr Ser Ala Asp Thr Pro Ser Ser Tyr Thr Gln Ser Thr  
340 345 350

atg gat cat gat ctt cat gat gct ctg tagaaaaat gaaatggta	1282
Met Asp His Asp Leu His Asp Ala Leu	
355	360
aatgcagagt caatgaactt ttccacattc agagcttact taaaaattgg tatttttagg	1342
taagagatcc ctgagccagt gtcaggagga aggcttacac ccacagtgga aagacagctt	1402
ctcatcctgc aggtagcttt ttctctccca ctagacaagt ccagcctggc aagggttcac	1462
ctgggctgag gcaccccttcc tcacaccagg ctgcctgca ggcacatgatc agtctgatga	1522
gaactctgag cagtgcgttga atgaagttgt agttaatatt gcaaggcaaa gactattccc	1582
ttctaacctg aactgatggg tttctccaga gggatttgcg gactactggc tgatggagta	1642
aatcgctacc tttgctgtg gcaaattggc ccccg	1677

<210> 34

<211> 360

<212> PRT

<213> Homo sapiens - human CCR4

<400> 34

Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr

1 5 10 15

Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu  
20 25 30

Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu  
35 40 45

Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu  
50 55 60

Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn  
65 70 75 80

Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly  
85 90 95

Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met  
100 105 110

Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val  
115 120 125

Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe  
130 135 140

Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala  
145 150 155 160

Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser  
165 170 175

Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser  
180 185 190

Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile  
195 200 205

Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met  
210 215 220

Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala  
225 230 235 240

Val Lys Met Ile Phe Ala Val Val Leu Phe Leu Gly Phe Trp Thr  
245 250 255

Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val  
260 265 270

Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala  
275 280 285

Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr  
290 295 300

Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys  
305 310 315 320

Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln  
325 330 335

Ile Tyr Ser Ala Asp Thr Pro Ser Ser Tyr Thr Gln Ser Thr Met  
340 345 350

Asp His Asp Leu His Asp Ala Leu  
355 360

<210> 35  
<211> 1784  
<212> DNA  
<213> murine MDC cDNA

<220>  
<221> CDS  
<222> (1) .. (276)

<220>  
<221> mat\_peptide  
<222> (73)..(276)

<400> 35

atg tct aat ctg cgt gtc cca ctc ctg gtg gct ctc gtc ctt ctt gct 48  
Met Ser Asn Leu Arg Val Pro Leu Leu Val Ala Leu Val Leu Ala  
-20 -15 -10

gtg gca att cag acc tct gat gca ggt ccc tat ggt gcc aat gtg gaa 96  
Val Ala Ile Gln Thr Ser Asp Ala Gly Pro Tyr Gly Ala Asn Val Glu  
-5 1 5

gac agt atc tgc tgc cag gac tac atc cgt cac cct ctg cca tca cgt 144  
Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His Pro Leu Pro Ser Arg  
10 15 20

tta gtg aag gag ttc ttc tgg acc tca aaa tcc tgc cgc aag cct ggc 192  
Leu Val Lys Glu Phe Phe Trp Thr Ser Lys Ser Cys Arg Lys Pro Gly  
25 30 35 40

gtt gtt ttg ata acc gtc aag aac cga gat atc tgt gcc gat ccc agg 240  
Val Val Leu Ile Thr Val Lys Asn Arg Asp Ile Cys Ala Asp Pro Arg  
45 50 55

cag gtc tgg gtg aag aag cta ctc cat aaa ctg tcc tagggaggag 286  
Gln Val Trp Val Lys Lys Leu Leu His Lys Leu Ser  
60 65

*11*  
gacctgatga ccatgggtct ggtgtggtcc agggaggctc agcaagccct attcttctgc 346

cattccagca agagccttgc caacgacgcc acctttactc acctccatcc cctgggctgt 406

cactctgtca ggctctggtc cctctacctc ccctctatcc cttccagctt atcccccttc 466

aatgtggcag ctgggaaaca cattcaggcc agccttaccc aatgcctact ccccaactgct 526

ttagatgaga ccagcgtcct tggggatg ccctgatcct atgatgcctt ccccatcccc 586

agccttggcc cccttctt cttgcattgtt gggaggccc ataggtttca aatatgtgt 646

acctacttcc ctttctgggg ggttctaata cccagcatgt tttcctgtt gcaggcacct 706

atccagtgcc acacacccca caagtttcta tcagtccttccag tgggcattca ccaagccca 766

aacttcagac ttccttggcc tccacctact ctcagtagaa ttctggagttt caggctgg 826

tccaccagggc ccccccagggt taggccaagg tccccaccag agtccttcctt gtttcttgg 886

ctgcagcactc gggcaggag caaggagcag gctcagaatc agatttctta aaggagctgc 946

agactccatc agtaaaagga atctttctcc catccctgaa tataaggcag ttttctgtca 1006

acacagagac tcaggttgtt agaaatggcc acatagatca actgtgaaac cctaaattta 1066  
ccaagaatca acttccaccc ctcttcaacc acatgctagg gtctttact ttctctgcc 1126  
cacaccttg actccttgcc tggtagctg atagtcgaag ttatgctatg gtgtcagtga 1186  
ctgccacagt ttgttggta ttataagcta tagttatatt tatataggaa agaggataaa 1246  
tatatgtggg ccaaataagac gaactggaga gttttaggat ctggggcag gaagggccat 1306  
acaaagtat acctcagaaa atagatggtt gtggagctg ctgcaagtgg cagatccaac 1366  
ttaaagaact taattgaaat tattcttgag tggctgaggc caagacaaga atatagaacc 1426  
cattcttgct tccctggaga caacagtggt cccaggggaa ggaataaaacc ttcttgctcc 1486  
tctggaggga gcatggcctg rcttagccga gtgactggac tgtgtgagat tgggggcatc 1546  
gctttcccty tctgagccctc agctgacagc atatggacc acaaaggct tgatccaaac 1606  
cacagggatt gacagtgcga gccacagctg tgtccagggc tcgtgttctg ccagaaggag 1666  
cacctggacg accagggcca ccactagtgc tactttgctc actgcccattg catgtcctga 1726  
aggcccctcc ccctcccttc ctacttctgg gaaaataaaat gctcgccaaat aatacctg 1784

*AI*  
<210> 36  
<211> 92  
<212> PRT  
<213> murine MDC

<400> 36

Met Ser Asn Leu Arg Val Pro Leu Leu Val Ala Leu Val Leu Ala  
-20 -15 -10

Val Ala Ile Gln Thr Ser Asp Ala Gly Pro Tyr Gly Ala Asn Val Glu  
-5 1 5

Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His Pro Leu Pro Ser Arg  
10 15 20

Leu Val Lys Glu Phe Phe Trp Thr Ser Lys Ser Cys Arg Lys Pro Gly  
25 30 35 40

Val Val Leu Ile Thr Val Lys Asn Arg Asp Ile Cys Ala Asp Pro Arg  
45 50 55

Gln Val Trp Val Lys Lys Leu Leu His Lys Leu Ser  
60 65

<210> 37  
<211> 958  
<212> DNA  
<213> rat MDC cDNA

<220>  
<221> CDS  
<222> (1) .. (243)

<220>  
<221> mat\_peptide  
<222> (40) .. (243)

<220>  
<221> misc\_feature  
<222> (206)  
<223> n = A or G or T or C

<220>  
<221> misc\_feature  
<222> (785)  
<223> n = A or G or T or C

<220>  
<221> misc\_feature  
<222> (827)  
<223> n = A or G or T or C

*AI*

<220>  
<221> misc\_feature  
<222> (836)  
<223> n = A or G or T or C

<220>  
<221> misc\_feature  
<222> (861)  
<223> n = A or G or T or C

<220>  
<221> misc\_feature  
<222> (864)  
<223> n = A or G or T or C

<220>  
<221> misc\_feature  
<222> (871)  
<223> n = A or G or T or C

<220>  
<221> misc\_feature  
<222> (878)  
<223> n = A or G or T or C

<220>  
<221> misc\_feature  
<222> (206)  
<223> n = A or G or T or C

<220>  
<221> misc\_feature  
<222> (882)  
<223> n = A or G or T or C

<220>  
<221> misc\_feature  
<222> (900)  
<223> n = A or G or T or C

<220>  
<221> misc\_feature  
<222> (902)  
<223> n = A or G or T or C

<220>  
<221> misc\_feature  
<222> (206)  
<223> n = A or G or T or C

<220>  
<221> misc\_feature  
<222> (907)  
<223> n = A or G or T or C

<220>  
<221> misc\_feature  
<222> (206)  
<223> n = A or G or T or C

<220>  
<221> misc\_feature  
<222> (916)  
<223> n = A or G or T or C

<220>  
<221> misc\_feature  
<222> (921)  
<223> n = A or G or T or C

<220>  
<221> misc\_feature  
<222> (951)  
<223> n = A or G or T or C



<210> 38

<211> 81

<212> PRT

<213> rat

<220>

<221> misc\_feature

<222> (56)

<223> Xaa = any or unknown amino acid

<400> 38

Leu Val Leu Leu Ala Val Ala Leu Gln Thr Ser Asp Ala Gly Pro Tyr  
-10 -5 1

Gly Ala Asn Val Glu Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His  
5 10 15

Pro Leu Pro Pro Arg Phe Val Lys Glu Phe Tyr Trp Thr Ser Lys Ser  
20 25 30 35

Cys Arg Lys Pro Gly Val Val Leu Ile Thr Ile Lys Asn Arg Asp Ile  
40 45 50

Cys Ala Asp Pro Xaa Met Leu Trp Val Lys Lys Ile Leu His Lys Leu  
55 60 65

Ala

OR  
<210> 39

<211> 506

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: S. cerevisiae alpha factor pre-pro/human MDC cDNA chimeric construct

<220>

<221> CDS

<222> (15) .. (476)

<220>

<221> mat\_peptide

<222> (270) .. (476)

<400> 39

atctcgagct cacg atg aga ttt cct tca att ttt act gca gtt tta ttc 50  
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe  
-85 -80 -75

gca gca tcc tcc gca tta gct gct cca gtc aac act aca aca gaa gat Ala Ala Ser Ser Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp -70 -65 -60	98
gaa acg gca caa att ccg gct gaa gct gtc atc ggt tac tta gat tta Glu Thr Ala Gln Ile Pro Ala Glu Ala Val Ile Gly Tyr Leu Asp Leu -55 -50 -45	146
gaa ggg gat ttc gat gtt gct gtt ttg cca ttt tcc aac agc aca aat Glu Gly Asp Phe Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn -40 -35 -30	194
aac ggg tta ttg ttt ata aat act act att gcc agc att gct gct aaa Asn Gly Leu Leu Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys -25 -20 -15 -10	242
gaa gaa ggg gta cct ttg gat aaa aga ggc ccc tac ggc gcc aac atg Glu Glu Gly Val Pro Leu Asp Lys Arg Gly Pro Tyr Gly Ala Asn Met -5 1 5	290
gaa gac agc gtc tgc cgt gat tac gtc cgt tac cgt ctg ccc ctg Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu 10 15 20	338
cgc gtg gtg aaa cac ttc tac tgg acc tca gac tcc tgc ccg agg cct Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro 25 30 35	386
ggc gtg gtg ttg cta acc ttc agg gat aag gag atc tgt gcc gat ccc Gly Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro 40 45 50 55	434
aga gtg ccc tgg gtg aag atg att ctc aat aag ctg agc caa Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln 60 65	476
tgaaggcctt ctagagcggc cgcatcgata	506

<210> 40  
<211> 154  
<212> PRT  
<213> cDNA

<400> 40  
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser  
-85 -80 -75 -70  
Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp Glu Thr Ala Gln  
-65 -60 -55

Ile Pro Ala Glu Ala Val Ile Gly Tyr Leu Asp Leu Glu Gly Asp Phe  
-50 -45 -40

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu  
-35 -30 -25

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val  
-20 -15 -10

Pro Leu Asp Lys Arg Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val  
-5 1 5 10

Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys  
15 20 25

His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu  
30 35 40

Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Trp  
45 50 55

Val Lys Met Ile Leu Asn Lys Leu Ser Gln  
60 65

<210> 41

<211> 93

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human MDC Analog

*AB* (

<220>

<221> misc\_feature

<222> (2)

<223> Xaa = not proline

<400> 41

Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val Leu Val Leu Ala  
-20 -15 -10

Val Ala Leu Gln Ala Thr Glu Ala Gly Xaa Tyr Gly Ala Asn Met Glu  
-5 1 5

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg  
10 15 20

Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly  
25 30 35 40

Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg  
45 50 55

Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln  
60 65

<210> 42  
<211> 538  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (53) .. (334)

<220>  
<221> mat\_peptide  
<222> (122) .. (334)

<400> 42  
ccctgagcag agggacctgc acacagagac tccctcctgg gtcctggca cc atg gcc 58  
Met Ala

cca ctg aag atg ctg gcc ctg gtc acc ctc ctc ctg ggg gct tct ctg 106  
Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Gly Ala Ser Leu  
-20 -15 -10

cag cac atc cac gca gct cga ggg acc aat gtg ggc cgg gag tgc tgc 154  
Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu Cys Cys  
-5 1 5 10

ctg gag tac ttc aag gga gcc att ccc ctt aga aag ctg aag acg tgg 202  
Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Thr Trp  
15 20 25

tac cag aca tct gag gac tgc tcc agg gat gcc atc gtt ttt gta act 250  
Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe Val Thr  
30 35 40

gtg cag ggc agg gcc atc tgt tcg gac ccc aac aac aag aag gtg aag 298  
Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg Val Lys  
45 50 55

aat gca gtt aaa tac ctg caa agc ctt gag agg tct tgaaggctcc 344  
Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser  
60 65 70

tcaccccaaga ctcctgactg tctccggga ctacctggga cctccaccgt tgggtttcac 404  
cgccccccacc ctgagcgcct gggtccaggg gaggccttcc agggacgaag aagagccaca 464

gtgagggaga tcccatcccc ttgtctgaac tggagccatg ggcacaaagg gcccagatta 524  
aagtctttat cctc 538

<210> 43  
<211> 94  
<212> PRT  
<213> Homo sapiens

<400> 43  
Met Ala Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Gly Ala  
-20 -15 -10  
  
Ser Leu Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu  
-5 1 5  
  
Cys Cys Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys  
10 15 20 25  
  
Thr Trp Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe  
30 35 40  
  
Val Thr Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg  
45 50 55  
  
Val Lys Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser  
60 65 70

<210> 44  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 44  
atgggaccat atggagcaaa tatggaagat agt 33

<210> 45  
<211> 335  
<212> DNA  
<213> Macaque MDC  
  
<220>  
<221> CDS  
<222> (19) . . (297)

<400> 45

agacatacag gacagagc atg gct cgc cta cag act gtg ttc ctg ggt gtc 51  
Met Ala Arg Leu Gln Thr Val Phe Leu Gly Val  
-20 -15

ctc atc ctc ctt gct gtg gcg ctt caa gca act gag gca ggc ccc tat 99  
Leu Ile Leu Leu Ala Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr  
-10 -5 1

ggc gcc aac atg gaa gac agc gtc tgc tgc cgt gat tac gtc cgt tac 147  
Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr  
5 10 15

cgt atg ccc ctg cgt gtg aaa cac ttc tac tgg acc tca gac tcc 195  
Arg Met Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser  
20 25 30 35

tgc ccg agg cct ggc gtg gtg ttg cta acc tcc agg gat aag gag atc 243  
Cys Pro Arg Pro Gly Val Val Leu Leu Thr Ser Arg Asp Lys Glu Ile  
40 45 50

tgt gcc gat ccc aga gtg ccc tgg gtg aag atg att ctc aat aag ctg 291  
Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu  
55 60 65

agc caa tgaagagcct actatgatga ccgtggccta agcaagcc 335  
Ser Gln

<210> 46

<211> 93

<212> PRT

<213> Macaque MDC

<400> 46

Met Ala Arg Leu Gln Thr Val Phe Leu Gly Val Leu Ile Leu Leu Ala  
1 5 10 15

Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu  
20 25 30

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Met Pro Leu Arg  
35 40 45

Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly  
50 55 60

Val Val Leu Leu Thr Ser Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg  
65 70 75 80

Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln  
85 90